

GenCore version 5.1.4.D5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_nzp model

Run on: May 7, 2003, 15:14:59 ; Search time 33 Seconds  
(without alignments)  
5798.990 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257

Perfect score: 6089  
Sequence: 1 atgcggcgccatgcggggcct.....aagaagcagcaggggtctga 3252

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL-frame+npz.model -DEV-  
-O/cgn2\_1/USPTO.spool/US09965830/runat.07052003.151450.6292/app.query.fasta\_1.3399  
-DB-Issued\_Patents\_AA -QFMT-Fastan -SUFFIX-rai -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE-pct -THR MAY=100 -THR MIN=0 -ALIGN=15  
-MODE-LOCAL -OUTFMT-pio -NORM-ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER-US09965830 @cgn2\_1.1.50.6runat.07052003.151450.6292 -NCPU=6 -ICPU=3  
-NO\_XLPRX -NO\_MMAP -LARGEOUTER -NEG\_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=1  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	5704	93.7	1083	4	US-09-600-776-2
2	5698	93.6	1083	4	US-09-343-494-1
3	5649.5	92.8	1082	4	US-09-336-643A-20
4	2461.5	40.4	1017	4	US-09-600-776-6
5	1901	31.2	1284	4	US-09-343-494-9
6	1551	25.5	1159	2	US-08-956-242-13
7	1551	25.5	1159	3	US-09-351-215-13
8	1551	25.5	1159	4	US-09-226-012-2
9	1551	25.5	1159	4	US-09-226-012-2
10	1120.5	18.4	888	2	US-08-956-242-4
11	1120.5	18.4	888	3	US-09-351-215-4
12	817.5	13.4	626	2	US-08-956-242-2

13	817.5	13.4	626	3	US-09-351-215-2	Sequence 2, Appl
14	417	6.8	1064	1	US-08-642-255-62	Sequence 62, Appl
15	410	6.8	960	4	US-09-219-849-5	Sequence 5, Appl
16	409	6.8	1065	1	US-08-642-255-72	Sequence 72, Appl
17	403.5	6.7	1065	1	US-08-642-255-80	Sequence 80, Appl
18	403.5	6.7	1065	3	US-08-642-246-16	Sequence 16, Appl
19	403.5	6.7	1065	4	US-09-451-206-16	Sequence 16, Appl
20	403.5	6.7	1065	5	PCR-US96-06229-16	Sequence 16, Appl
21	399.5	6.6	960	4	US-09-219-849-6	Sequence 6, Appl
22	399	6.6	1008	4	US-09-219-849-6	Sequence 8, Appl
23	396	6.5	1461	4	US-09-585-887-9	Sequence 9, Appl
24	396	6.5	1461	4	US-09-585-887-9	Sequence 9, Appl
25	389.5	6.4	960	4	US-09-289-578-9	Sequence 9, Appl
26	387	6.4	1057	3	US-08-931-820-1	Sequence 5, Appl
27	384.5	6.3	777	1	US-08-642-255-53	Sequence 1, Appl
28	381	6.3	1065	1	US-08-642-255-72	Sequence 53, Appl
29	379.5	6.3	1064	1	US-08-642-255-62	Sequence 72, Appl
30	377.5	6.2	1064	1	US-09-585-887-9	Sequence 62, Appl
31	377.5	6.2	1461	4	US-09-585-887-9	Sequence 9, Appl
32	366	6.0	720	4	US-09-219-849-4	Sequence 9, Appl
33	362	5.9	1917	4	US-09-627-650B-5	Sequence 4, Appl
34	362	5.9	1917	4	US-09-436-063C-5	Sequence 5, Appl
35	358.5	5.9	1057	3	US-08-931-820-1	Sequence 5, Appl
36	358.5	5.9	1341	3	US-08-963-825-18	Sequence 18, Appl
37	358.5	5.9	1341	4	US-09-500-811-18	Sequence 18, Appl
38	358.5	5.9	1341	4	US-08-963-825-18	Sequence 18, Appl
39	358.5	5.9	1341	4	US-09-570-573-18	Sequence 18, Appl
40	351	5.8	1652	4	US-09-548-608-18	Sequence 18, Appl
41	351	5.8	1652	4	US-09-627-650B-1	Sequence 1, Appl
42	349.5	5.8	1652	4	US-09-436-063C-1	Sequence 1, Appl
43	349.5	5.8	1341	3	US-08-963-825-18	Sequence 18, Appl
44	349.5	5.8	1341	4	US-09-500-811-18	Sequence 18, Appl
45	349.5	5.8	1341	4	US-09-570-573-18	Sequence 18, Appl
					US-09-548-608-18	Sequence 18, Appl

## ALIGNMENTS

RESULT 1  
US-09-600-776-2  
Sequence 2, Application US/09600776  
Patent No. 6326168  
GENERAL INFORMATION:  
APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
TITLE OF INVENTION: A novel potassium channel protein  
FILE REFERENCE: Y9903-PCT  
CURRENT APPLICATION NUMBER: US/09/600,776  
CURRENT FILING DATE: 2000-07-21  
PRIOR APPLICATION NUMBER: JP P1998-011434  
PRIOR FILING DATE: 1998-01-23  
PRIOR APPLICATION NUMBER: JP P1998-346198  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 1083  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-600-776-2

Alignment Scores:  
Pred. No.: 0  
Score: 5704.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 93.68%  
DB: 4  
Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-600-776-2 (1-1083)  
QY 1 ATGCGGCGCAGCGGGGCGCTCTGCGCGCTGAGACACCTTCTGAGACCATCGCTACG 60  
DB 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY	61	CGCTTCAGCGGACGACGACAGTAACTTGCTGCTGGGCAAGCCGACGGTGGGGGCTTC	120
Db	21	ArgpheasprgylThrHisSerAspPheValIleuclYasnaGlInValAlaGlyLeuPhe	40
QY	121	CCCGTGGTAACTCTGATGGGCTTGACACTCAAGGCTTCCTCCGGGTGAAGTC	180
Db	41	ProValValTyrCysSerAspGlyPheCysAspLeuThrLeuPheSerAlaGluVal	60
QY	181	ATGAGGGGGGCTGGCTGCTCTCTCTTATGGGCGAGACACAGTGAAGCTGCTGGC	240
Db	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrclProAspThrSerGluLeuValArg	80
QY	241	CAACAGATCCGCAAGGCCCTGAGAGACGACACAGAGATTCAAGGCTGAGCTGTAC	300
Db	81	GlnGlnIleArgLysAlaLeuAspGlnHisLysGluPheLysAlaGluLeuIleLeuTyr	100
QY	301	CGGAGAGCGGGCTCCGCTTGCTGCTGCTGGATGGATACCCATTAAGAAAGAGAA	360
Db	101	ArgLysSerGlyLeuProPheThrPheLysLeuAspValIleProIleLysAsnGluLys	120
QY	361	GGGAGAGTGGCTCTTCTTCTAGTCTCCACAAAGGACATCAGCAAGCAACCAAGGAGG	420
Db	121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140
QY	421	GGCCCCAGATGGAGAGACAGTGGTGGCCGCGCCGATATGGCCGGGACGATCC	480
Db	141	GlyProAspArgTyrLysGluThrclYelYelYarArgArgTyrGlyArgAlaArgSer	160
QY	481	AAAGGCTTCATGCCAACCGGGGGGAGCCGGGCGGTCTACCACCTGTCCGGGAC	540
Db	161	LysGlyPheAsnAlaAsnArgArgArgSerArgAlaValIleuTyrHisLeuSerLHis	180
QY	541	CTGCAGACGAGCCCAAGGGCAAGACACAAAGCTCATTAAGGGGCTTTGGGAGAAACA	600
Db	181	LeuGlnLysGluProLysGlyLysHisLysLeuAsnLysGlyValPheGlyLysPro	200
QY	601	AACTTCCCTGATACAAAGTAGCGGCAATCCGGAATGCCCTTATCCTGTGCACTGT	660
Db	201	AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys	220
QY	661	GGGGCACTGAGACCCACCTGGGATGGCTTCATCTGCTGCGCACACTATGTGGCTGTC	720
Db	221	GlyAlaLeuArgValaThrThrAspArgLysPheIleLeuLeuAlaThrLeuTyrValAlaVal	240
QY	721	ACTGTGCGCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGTCCCGCGGGCCGG	780
Db	241	ThrValProItyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
QY	781	CCCAGGCTGTGACCTGGCCGCTGGAGGTCCTTTATCTTGATCTTGCGTGAATTTC	840
Db	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPro	280
QY	841	CGTACCAATTCGTGTGCCAAGTGGGGGAGGTGGTGTTCGCCCAAGTCCATTTGCTTC	900
Db	281	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu	300
QY	901	CACACTGTACACACTGGTCTCTGCTGATGATCATCGACAGCGTGGCCTTGTGACTGTA	960
Db	301	HisTyrValThrThrTyrPheLeuLeuAspValIleAlaIleLeuProPheAspLeuLeu	320
QY	961	CATGCTTCAAGTCAACGTGTACTTGGGGGCCCATGCTGTGAAGAGGTGGCGCTGCTG	1020
Db	321	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	340
QY	1021	CGCTGTGCGCCTGTTCGCGGGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTCTG	1080
Db	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360
QY	1081	ACACTGCTCATGGCCGCTGTGGCCCTGCTGCGCAGTACAGCGCCGTGGTCTTAC	1140
Db	361	ThrLeuLeuMetAlaValAlaPheAlaLeuLeuAlaHisTyrValAlaCysValThrPheTyr	380
QY	1141	ATTGGCCAGCGGAGATCGAAGACGAGCAATCCGAGCTGCTGTGATTGGCTGGCTCAG	1200

Db	381	llegylgnarglnlleglnserserglnserglnleuproglnlleglytripleu	400
OY	1201	GAGCTGGCCGGCGACTGGAGACTCCCTACTACCTGTGTGGGCGGAGGCCAGCTGGAGG	1260
Db	401	glnleualatargtrleuglnluthrprolytryleualgtrargproalaglly	420
OY	1261	AACAGCTCCGGCGAGATGATACACTGACAGCAGCAGCAGGAGGCCAGCGGAGGGGTG	1320
Db	421	asnserserglyninsertspansncyserserserserglnlalaanglythrglyleu	440
OY	1321	GAGCTGCTGGGGCGCCGTGCGTGGCGAGCGGCTACATCACTCCCTCTACTTGGCACTC	1380
Db	441	glnleuleuglyserproserleuargseralatyrllethrseryleuylrhealaleu	460
OY	1381	AGCAGCTCACACAGCTGGGCTTCGGCAACGTGTCCGCCACACAGGACCCAGAGAATC	1440
Db	461	serserleuthrservalglyrheglyaanaValseralaastrhrasphrlnustyle	480
OY	1441	TTGTCAATGACACATGGTCATCGGCGCCCTGATGCACGCGGTGTGTGGAACTG	1500
Db	481	pheserleuystrmetleuilegylalalemethlalaValalrheglysnaVal	500
OY	1501	ACGGCCATCATCCAGGCGATGTAGCGCCCGCGCTTCTGTACACAGCCGACGCGGAC	1560
Db	501	ThrAlaIleIleGlnargmetlyrAlaargArgPheleuThylsserarghrargaar	520
OY	1561	CTGGCGCACTACATCGGATCCACCGTATCCCAAGCCCTCAAGAGGGCATGCTGGAG	1620
Db	521	leuargspurylleargilehlsarglleprolysproleuysglnargmetleugln	540
OY	1621	TACTTCCAGGCCACTGGGGGGGTGAACAATGGGATGACACACGAGGCTGCGCAGAC	1680
Db	541	tyrPheGlnAlaThrTrpAlaValaAlasnaanglyleasphrthrleuileuenglnser	560
OY	1681	CTCCCTGACAGCGGCGCGGACATCGCATCGCATCGCATCGACAAGAGGTCTGCAGT	1740
Db	561	leuprosargglnleualargalaasrlylalemethlssleuhslysglvalleuglnleu	580
OY	1741	CCACTGTTTGAAGCGCGCAGCGCGGCGGTGCTGGCGGCACTGTCTTGCGCTGCGGCC	1800
Db	581	ProleupheglnAlaAlaIaseraArgglyCyaleuarglaleuSerleuAlaleuAargpro	600
OY	1801	GCTTTGTCACAGCGCGGCGAGTACCTCATCCACAGGCGATGCGCTGCGAGCCCTTAC	1860
Db	601	AlaPheCysThrproglyglnTytleuilehlsinglnlaspAlaleuGlnAlaleuTy	620
OY	1861	TTTGTCTGCTGGCTCCATGGAAGGTGCTCAAGGTGGCAACCGTGCACCACTGAGG	1920
Db	621	PheValCysserglysermetleuValleuysglglythrValleualalleuilegly	640
OY	1921	AAGGCGCACTGATCGGTGTGAGCTGCGCGGCGGAGCGAGGTGTAAGAGCCATAGCC	1980
Db	641	lysglyasrPheIleIleglyCyseglleuProlargtrglnleuValValylvalaasnaVal	660
OY	1981	GACGGGAAGGGGTACACTAGCTGCTGTGCAAGTGTGTGCACTGGGTGGCTGCAGAC	2040
Db	661	asrvallysglyleuthrTyrcysValleuenglnCysleuGlnleualaglyleuhsiasr	680
OY	2041	AGCTTTCGCTTACCCGAGTTTGCACCCGCGCTTCACTGCTGGCTTCGAGGGAGCTC	2100
Db	681	serleualaleuTyrrprogluphealProlargPheaserargglyleuargglyleu	700
OY	2101	AGCTACACCTGGGTGTGGGGGAGGCTGTGCAGAGGTGGACACACAGTCCCTTGAAGGCG	2160
Db	701	serTyraasleuGlyAlaglylyglseralaglnValasrPthserSerleuSerlely	720
OY	2161	GACATACCTTATGTCCAGCTGGAGAGAGAAGAGACAGATGGGGAGACAGGGCCCCAG	2220
Db	721	AspAsnThrleuMetserThrleuenglnGlnlysglnThrAspGlyglnleuGlyProThr	740
OY	2221	GTGTCCCAAGCCCACTGATAGCGCTCACCCCTGCTGTCCCTGGGTGCACTCC	2280

D	741	ValSerProAlaProAlaAspLysProSerSerProLeuLeuSerProGlyCysThrSer	760
Q	2281	TCATCTCAAGCTGCCAAAGCTGTCTATCCCACTGCAGACAGACCCCGGCTCCGTACGT	2340
D	761	SerSerSerAlaAlaLysLeuSerProAlaGlyThrAlaProAlaProAlaGluLys	780
Q	2341	GGCAGAGGAGGCCAGGACGGGCGACGGGCTTTGAAGGCTGAGGCTGGGCTGTGCTGCC	2400
D	781	GlyAlaGlyAlaArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	800
Q	2401	CCACGGGCGCTTGAGGGGCTACGGTGGCCCCCATTCACATCCATGGAATGTGCCCCAGATCTG	2460
D	801	ProAlaGlyAlaLeuGlyLysLeuArgLeuProProMetProIleProAlaValProProAspLeu	820
Q	2461	AGCCCAAGGAGTAGAGAGGATTTGAAGACGGCTGTGGCTCGGACCAAGCCCAAGTTCTCT	2520
D	821	SerProAlaGlyValAlaAspGlyIleGluAspLysLysSerAspGlnProLysPheSer	840
Q	2521	TTTCGGCTGGGCGCACTGGGCGCGGAATTGAGACAGACCCCTCCCTGGACCAAGAGAC	2580
D	841	PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer	860
Q	2581	GGCTGCGCACTGTTCCCAATGGGCGCCAGGAGGCAAGAACAGACACATCTGACAAAG	2640
D	861	GlyLeuLeuThrValProAlaHisGlyProSerGlyAlaArgSerThrAspThrLeuAspLys	880
Q	2641	CTTGGCAGAGCGGCGACAGAGCGTGTGAGACAGCTGTGAGATGCGGGAGAGCATGCAAG	2700
D	881	LeuArgGlnAlaValThrGlyLeuSerGlyGlnValLeuGlnMetArgLysGlyLeuGln	900
Q	2701	TCACTTGGCAAGCTGTGCAGCTTGTCTGTGGCGCCACAGGAGGAGGTCGGTCCCTCGG	2760
D	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProAlaHisArgGluLysProCysProArg	920
Q	2761	GCATGGGAGAGGGGCGGCTGCCAGCCAGACACTCCGGGCTTCTGACGCTGTGTGG	2820
D	921	AlaSerGlyGluLysProCysProAlaSerThrSerGlyLeuGlnProLeuCysVal	940
Q	2821	GACACTGGGGACCTCTCACTGCGCTGGAGCCGCCACAGCTGTGTCTTGAAGTGGAGCT	2880
D	941	AspThrGlyAlaSerSerLysLysLeuGlnProProAlaGlySerValLeuSerGlyThr	960
Q	2881	TGGCCCAACCTGTCCGGGGGCTCTCCCTCATGAGCAACCTGGGCGCTGGGGTCCCCA	2940
D	961	TyrProHisProArgProGlyProProProLeuMetAlaProTyrProTyrGlyProPro	980
Q	2941	GGGTCAAGAGCTCCCGCTGGCTGAGCCCAAGCTTCTGAGACTCCACTCAAGTCA	3000
D	981	AlaSerGlnSerSerProTyrProAlaGlyAlaThrIleThrIleThrIleSerThrSerAspSer	1000
Q	3001	GAGCCCGGCTGAGGAGACTCTGTCTGTAGCCCAAGCAACCTGCTCCCTCTCTCT	3060
D	1001	GluProProAlaSerGlyAspLeuLysSerGluProSerThrProAlaSerProProPro	1020
Q	3061	TCTGAGAGGGGCTAGAGACTGGGGCGCCAGAGGCTGTGAGCCAGGCTGAGGCTACAGC	3120
D	1021	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1040
Q	3121	ACTGAGAGCCCAACAGAGGTCAAGGGGCTGAGGGGCTGTGGCTGGAGCCCAAGGCTG	3180
D	1041	ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTyrAspProHisSerLeu	1060
Q	3181	GAGATGGCTTATTTGGCTGCAATGAGCTGTGCAAGTCCAGTGAAGCAAGAGAGG	3240
D	1061	GluMetValLeuLeuGlyCysHisGlySerGlyThrValGlnThrThrGlnGluGluGly	1080

```

: Patent No 6413741
:
: GENERAL INFORMATION:
:
: APPLICANT: Jegla, Timothy J.
: APPLICANT: Wickenden, Alan
: APPLICANT: ICAGEN, Incorporated
: TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
: FILE REFERENCE: 018512-00132005
: CURRENT APPLICATION NUMBER: US/09/343,494
: EARLIER FILING DATE: 1999-06-30
: EARLIER APPLICATION NUMBER: US 60/091,469
: EARLIER FILING DATE: 1998-07-01
: EARLIER APPLICATION NUMBER: US 60/116,621
: EARLIER FILING DATE: 1999-01-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 1
:
: LENGTH: 1083
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: OTHER INFORMATION: human Elk (hElk; Eag (eag) gene)
: OTHER INFORMATION: potassium channel monomer protein
US-09-343,494-1

```

```

Alignment Scores:
Pred. No.:      0      Length:      1083
Score:          5698.00 Matches:      1082
Percent Similarity: 99.91% Conservative: 0
Best Local Similarity: 99.91% Mismatches: 1
Query Match:      93.58% Indels:      0
DB:              4      Gaps:      0

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-343-494-1 (1-1083)

```

Qy	1	ATGCGGGCCATTGGGGGGGCTCCCTGGCGCTCAGAAACACCTTCCTGGACACCATGCTACG	60
Db	1	MeCProlaMeIetrGgLyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
Qy	61	CGGTCGACGGCAGCAGCAGTAACCTCGCTGGGCGAACGCCAGGTGGCGGGCTCTTC	120
Db	21	ArgPheAspCpLyrThrIleSerSerAspPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe	40
Qy	121	CCCGTGGTACTGCTCTATAGTGGCTTCGTGTGACCTCAGGGGCTTCTCCCGGCTGAGTC	180
Db	41	ProValValTyrCysSerAspCpLyrPheCysAspLeuThrGlyPheSerArgAlaGlyVal	60
Qy	181	ATGCACGGGGGCTGTGCTGCTCTCTCCCTTATGAGCGCAGACACAGAGAGCTGTCCG	240
Db	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGlyLeuValArg	80
Qy	241	CAACAGATCCGACAGCCCTGGACAGCAGCAGACAGAGAGTTCAGGCTGAGCTGATCTGTAC	300
Db	81	GlnGlnIleLeuTyrGlyAlaLeuAspCpLyrIleTyrGlyPheTyrAlaGlyLeuIleTyr	100
Qy	301	CGAAGAGGGGGCTCCCTTCCTGTGTCTCTGATGTGATACCATTAAGATGAGAA	360
Db	101	ArgLysSerGlyLeuProPheTrpCysLeuLeuAspAlaIleProIleLysAsnGlyLys	120
Qy	361	GGGAGGTGGCTCTTCTAGTCTCTCCACAAAGACATCAGCGAAACCAAGAACCGAGG	420
Db	121	GlyGlyValAlaLeuPheLeuValSerHisLysSprLleSerGlyThrLysAsnArgGly	140
Qy	421	GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCCGAGATAGCGCGGACGATCC	480
Db	141	GlyProAspArgTrpLysGlyThrIleGlyLysArgArgTyrGlyArgAlaArgSer	160
Qy	481	AAAGCTTCAATGGCCAAACGGCGCGGAGCGCGGCGTGTCTACCAACTGTCCCGGAC	540
Db	161	LysGlyPheAsnAlaAsnArgArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180
Qy	541	CTGAGAGAAGACGCCCAAGGGCAGACCAAGCTCATTAAGGGGGCTTTGGGAGAAACA	600
Db	181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValaPheGlyLysLysPro	200

QY	601	AACCTGGCTAGATCAAAAGTACGCCCATCGGAAAGTCGGCCCTTCAATCGTGTGGACTGT	660
DB	201	AsnLeuProGluTyrUlysValAlaAlaIleTyrGlySerProPheIleLeuIleHisCys	220
QY	661	GGGGCACTGAGACCCACCTGGGAGTGGCTTCAATCCCGCGGCAACATGATGTGGCTGC	720
DB	221	GlyAlaLeuArgAlaThrTTPRAspOlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240
QY	721	ACTGTGCCCCACAGCGTGTGTGTGGACACACAGCGAGCCAGTCGCGCCGGCGGCCG	780
DB	241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
QY	781	CCGACGGCTGTGACCTGAGCGGTGGAGGTCTCTTCACTCTTGACATTTGCTGAATTC	840
DB	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAspPhe	280
QY	841	CGAACACATGTGTGTCCAAATCGGGGCCAGGTGTGTGTGCCCCAAAGTCCATTTGGCTC	900
DB	281	ArgThrThrPheValSerTyrSerGlyValValAlaPheAlaProLysSerIleCysLeu	300
QY	901	CACATACGTACACACTGTGTCTGTGTGTGATGTGCATCGACAGCGGCTCGCCCTTGACCTGTA	960
DB	301	HisTyrValThrThrPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	320
QY	961	CATGCTTCAAGTCAAGTGTACTTCGGGGGCCAATCTGTCAAGACGGTGGCGCTGTG	1020
DB	321	HisAlaPheUlysValAsnValTyrPheGlyAlaHisLeuLeuUlysThrValArgLeuLeu	340
QY	1021	CGGCTGTGGCGCTGTCCGCGCGGCGGCGGACCGGTACTGTCCAGTACACGCGCGTGTGTG	1080
DB	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGluTyrSerAlaValValLeu	360
QY	1081	ACACTGTCTATGGCCGTGTGTGCGCCCTGTGCGCACTGGGTGGCTGTGCTGTGTTC	1140
DB	361	ThrLeuLeuMetAlaValAlaPheAlaLeuLeuAlaHisTyrValAlaCysValTyrPheTyr	380
QY	1141	ATTGGCCAGCGGAGATCGAAGACAGCGAATCCGAGTGGCTGTGAGATGGCTGGCGGCA	1200
DB	381	IleGlyGlnArgGluIleGlnSerSerGlnSerGluLeuProGluIleGlyTyrPheGln	400
QY	1201	GAGTGGCGCGGCACCTGGAGACATCCCTACTACCTGTGGGCGGAGGCCACGCTGGAGGG	1260
DB	401	GluLeuAlaArgAlaGlyLeuGlnTyrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
QY	1261	AACAGCTCCGGCGAGAGTACACTGTGACGACGACGACGACGACGAGGCCAAGCGGAGGCTG	1320
DB	421	AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu	440
QY	1321	GAGCGCTGGGCGGCGGCTGTCTGCGGACGCGCTACATCACCTCCCTTACTTGCACTC	1380
DB	441	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460
QY	1381	AGCAGCTCACACAGCGTGGGCTTGGCAACGTGTCCGCAACGTGTCCGCAACAGGACACCGCAAAAGTCC	1440
DB	461	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGlnIleSle	480
QY	1441	TTTTCGATCTGCACATGTGTCTATGCGGCGGCTGATGCAAGCAAGGCGTGTGGGAACGTG	1500
DB	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal	500
QY	1501	ACGGCCATCATCAGCGGCACTGTAAACCGCGCGGCTTCTGTACACACAGCGGACGCGGCGAC	1560
DB	501	ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAsp	520
QY	1561	CTGCGGCACTAATCCGAGTCCACCGTATCCCAAGGCCCTTCAAGACGCGCATGTGTGAG	1620
DB	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGln	540
QY	1621	TACTTCAGGCGCACTGTGGCGGTGAACAATGGCATGCACACACGAGTGTGTGAGAC	1680
DB	541	TyrPheGlnAlaThrTTPRAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560

QY	1681	CTCCCTGCAGAGCTGCGCGGACAGACATCCGATCGACTGTGACAAAGAGGGCTCGACGTCT	1740
Db	561	LeuProAspArgIuLeuAlaArgAlaAspIleAlaMetHisLeuNH1sArgSGLuValLeuGlnLeu	580
QY	1741	CCACTGTTTGAAGGGGCGCACAGCCGGGGGCGTGGGCGACTGTCTCGGCGCTCGCGGCC	1800
Db	581	ProLeuPheGlnAlaIaIaSerArgGlyCysLeuNrgAlaLeuSerLeuAlaLeuArgPro	600
QY	1801	GGCTTCGACGCGCGGGGAGTACTATCCACACCAAGCGCATGGCTTCGACAGCCCTTAC	1860
Db	601	AlaPheCysThrProGlyIuLeuThrLeuHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
QY	1861	TTTGTCTGCTGCTGCGCTCCATGGAGGCTCTCAAGGTGGACCGCTGCTCGGCATCTAGG	1920
Db	621	PheValCysSerClySerMetGluValLeuLysGlyThrValLeuAlaIleLeuGly	640
QY	1921	AAGGGGACCTGATCGGCTGAGTGAAGTGGCCCGCGGGAGACAGGTGCTAAAGGCCAAAGCC	1980
Db	641	LysGlyAspLeuIleGlyCysGluLeuProArgArgGlnGlnValAlaLysAlaAsnAla	660
QY	1981	GACGTGAAGGGGCTGACGTACTGCTCTCGACAGTCTCGACGCTGGCGGGGCTCGACGAC	2040
Db	661	AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680
QY	2041	AGCTTCGCGCTGTAACCCGAGTTTGGCCCGGCGCTTCAGTCTGAGCTTCGAGGGAGCTC	2100
Db	681	SerLeuAlaLeuTyrProGluPheAlaProAlaPheSerArgGlyLeuArgGlyLeuLeu	700
QY	2101	AGCTACAACTGGGCTCTGGGGGAGGCTCTGCAGAGGTGACACACAGTCCCTGAGCGGC	2160
Db	701	SerTyrAsnLeuAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly	720
QY	2161	GACAAATACCTTATGTCCACGCTGAGAGAGAAAGAGACAGATGGGGAGACAGGGCCCAAG	2220
Db	721	AspAsnThrLeuMetSerThrLeuGlnGlnLysGlnThrAspLysGlyLeuIleNlyProThr	740
QY	2221	GCTCTCCCAAGCCCGAGCTATGAGCCCTCGAGCCCTGCGCCCTGCGCTGACACTCC	2280
Db	741	ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyLysThrSer	760
QY	2281	TGCATCTCAGCTGCACAGCTGATCCCACTCCGAAACAGACACCCCGGCTGCTAGGT	2340
Db	761	SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	780
QY	2341	GGCAGAGGAGGCGCAGGCGAGGGGCTTTGAAGGCTGAGGCTGCGCCCTCTGCTCCC	2400
Db	781	GlyArgGlyArgProGlyArgAlaGlyAlaLeuNlysAlaGluAlaGlyProSerAlaPro	800
QY	2401	CCACGGGCGCTAGAGGGGCTACGGCTGCGCCCGCATGCGAATGGCGCCCGACATCTG	2460
Db	801	ProArgAlaLeuGlnGlyLeuArgLeuProMetProThrPasnValProProAspLeu	820
QY	2461	AGCCCCAGGAGTATGATGGCATTTGAAGGGCGTGGGCGGACGACCCAGTTCTCT	2520
Db	821	SerProArgValValAspLysIleGlnAspLysCysLysSerAspGlnProLysPheSer	840
QY	2521	TTCCGCGTGGGCGATGCGGGCGGAAATGTAGCAGACGCCCTCCCTGGACGACAGAC	2580
Db	841	PheAlaGlyAlaGlyInSerIleProGlyCysSerSerSerProSerProGlyProGluSer	860
QY	2581	GGCGTCTACATGTTCCCATGGGCGCCACGAGGCAAGAAACACACACACTGGACAG	2640
Db	861	GlyLeuLeuThrValProHisGlyProSerGlnAlaArgAsnThrAspThrLeuAspLys	880
QY	2641	CTTCGCGCAGCGGTGACAGAGCTGTACAGACAGTGTCTGACAGTGGGAGGAGACTGACG	2700
Db	881	LeuArgGlnAlaValIleThrGluLeuSerGlnGlnValLeuGlnMetArgGlyLeuGln	900
QY	2701	TCACATTGCGCAGCTGTGACGTTGTCTTGGGGCGCCACAGGAGAGGTCGTGCGCTCGG	2760
Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGlyIleProCysProArg	920
QY	2761	GCAATCGGAGAGGGGCGCGTCCGCAAGCAGCAGCTCGGGCTTCTGACAGCTGTGTGTG	2820

```

Db 921 AAlaserGlyGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940
QY 2821 GACACTGGGGGACATCTCTCTACTGCTGCAGACCCAGCTGGCTCTGTAGTGGAGACT 2880
Db 941 AAspThrGlyAlaSerSerThrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960
QY 2881 TGGCCCCACCTGCTGCTGGGGGCTCTCTCCCTCATGGACCTGGCCCTGGGGTCCCA 2940
Db 961 TTPProHisProAlaProGlyProProProLeuMetaLAbProThrProThrGlyProPro 980
QY 2941 GCGCTCAGAGCTCCCGCTGGCTGCAGCCAGCTTGTGACCTCCACCTAGACTCA 3000
Db 981 AAlaserGlnSerSerProThrProAlaThrAlaPheThrThrSerThrSerAspSer 1000
QY 3001 GAGCCCCCTGCTCAGAGACCTCTGCTGTGAGCCAGCAGCCCTGCTCCCTCTCTCT 3060
Db 1001 GlnProProAlaSerGlyAspLeuGlySerGlnProSerThrProAlaSerProProPro 1020
QY 3061 TGTGAGAGAGGGGCTAGAGACTGGGCCCGCAGAGCTGTGAGCCAGCTGAGCTAGCTAC 3120
Db 1021 SerGlnGlnGlyAlaArgThrGlyProAlaGlnProValSerGlnAlaGlnAlaThrSer 1040
QY 3121 ACTGAGAGAGCCCCCAGCAGAGCTGAGAGGGGCTGGCTGGCTGGAGCCCAAGACCTG 3180
Db 1041 ThrGlyGlnProProProGlySerGlyGlyLeuAlaLeuProThrAspProHisSerLeu 1060
QY 3181 GAGATGATGCTATTGGTGGCCATGGCTGTGACACAGTCAATGACAGCCAGAGAGAGGC 3240
Db 1061 GlnMetValLeuLeuLeuGlyCysHisGlySerGlyThrValGlnThrGlnGlnGlnGly 1080
QY 3241 ACAGGGGCTC 3249
Db 1081 ThrGlyVal 1083

```

RESULT 3

```

US-09-336-643A-20
: Sequence 20, Application US/09336643A
: Patent No. 6399761
: GENERAL INFORMATION:
: APPLICANT: Miller, Andrew P.
: APPLICANT: Curran, Mark Edward
: APPLICANT: Hu, Ping
: APPLICANT: Rutter, Marc
: APPLICANT: Wang, Jian-Wang
: TITLE OF INVENTION: No. 6399761 Human Potassium Channels
: FILE REFERENCE: SEQ-15P
: CURRENT APPLICATION NUMBER: US/09/336,643A
: PRIOR APPLICATION NUMBER: 1999-06-18
: PRIOR FILING DATE: 1998-08-07
: PRIOR FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: 60/116,448
: PRIOR FILING DATE: 1999-01-19
: PRIOR APPLICATION NUMBER: PCT/US99/03826
: PRIOR FILING DATE: 1999-02-22
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 20
: LENGTH: 1082
: TYPE: PRT
: ORGANISM: H. sapiens
US-09-336-643A-20

```

Alignment Scores:

```

Pred. No.: 0
Score: 5649.50
Percent Similarity: 99.35%
Best Local Similarity: 99.35%
Query Match: 92.78%
DB: 4

```

```

Length: 1082
Matches: 1076
Conservative: 0
Mismatch: 6
Indels: 1
Gaps: 1

```

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-336-643A-20 (1-1082)

```

QY 1 ATGCGGCGCATGGGGGCTCTGCGCCCTCAGAACACTTCTCGACACCATCGTAGC 60
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTGACGGGACGACAGACTAACTTGTGCTGGGCAAGCCAGAGTGGCGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaSer---GlyGlyAlaLeu 39
QY 121 CCGGTGGTCAAGCTCTGATGCTGTGACCTCAGCGGCTTCTCCGGGCTGAGTTC 180
Db 40 ProValValTrpCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 59
QY 181 ATGACAGGGGGCTGTGCTCTCTCTCTCTTATGGGCGACACACAGTAGAGCTGTC 240
Db 60 MetGlnArgGlyCysAlaCysSerPheLeuTrpGlyProAspThrSerGlnLeuValArg 79
QY 241 CAACAGATCCGAGAGCCCTGAGACAGACAGAGAGTTCAAGGCTGAGTGCATGTAC 300
Db 80 GlnGlnIleArgGlyAlaLeuAspGlnHisGlyGlnPheLeuAlaGlnLeuIleLeuTr 99
QY 301 CGGAGAGCGGGCTCCGCTTGTGCTGTCTCTGATGTGATACCAATAAGATGAGAA 360
Db 100 ArgGlySerGlyLeuProPheThrPcySleLeuAspValIleProIleCysAsnGluTr 119
QY 361 GGGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 120 GlyGlnValAlaLeuPheLeuValSerHisCysAspIleSerGlnThrHisAsnArgGly 139
QY 421 GGGCGCGACAGATGAGAGAGAGAGAGTGTGCGCGCGCGCGATATGCGCGGACAGTCC 480
Db 140 GlyProAspArgTrpGlySerGlnThrGlyGlyArgArgArgGlyTrpArgAlaArgSer 159
QY 481 AAAGCTTCATATGCCAACCGCGCGGAGCGCGCGCGCTCTTACCACTGTCCGCGAC 540
Db 160 LysGlyPheAsnAlaAsnArgArgArgSerArgAlaValLeuTrpHisLeuSerGlyHis 179
QY 541 CTGCAAGAGCAGCCCAAGGGCAGAGCAAGCTCAATTAAGGGGCTGTGGGAGAAACA 600
Db 180 LeuGlnGlyGlnProGlySerGlyHisGlySleuAsnGlyGlyValPheGlyGlyLeuSpro 199
QY 601 AACTTGCCTGAGTACAAAGTACCGCGCATCGGAAGTGGCTTCAATCTGTGCACTGT 660
Db 200 AsnLeuProGlnTrpGlyValAlaIleArgGlySerProPheIleLeuLeuHisCys 219
QY 661 GGGGACAGAGAGCACTGGGATGGCTTCACTCTGCTGCCACACTATATGCTGTCT 720
Db 220 GlyAlaLeuAlaGlyAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTrpValAlaVal 239
QY 721 ACTGTGCCCTACAGGCTGTGTGAGCAGAGAGGGAGCCAGTGGCCGCGCGCGCG 780
Db 240 ThrValProTrpSerValCysValSerThrAlaArgGlnProSerAlaAlaArgGlyPro 259
QY 781 CCGACGCTGTGTGACCTGGCGGTGAGTCTCTCTCACTGATGTGATGTGTGAATTC 840
Db 260 ProSerValCysAspLeuAlaValGlnValLeuPheIleLeuAspIleValLeuAsnPhe 279
QY 841 CGTACACATTGCTGTCCAAAGTGGGCGAGGTGTGTGCGCCCAAGATCCATTGCTCTC 900
Db 280 ArgThrThrPheValSerGlySerGlyGlnValValPheAlaProGlySerIleLeu 299
QY 901 CACTACGTACACACTGCTGTCTGTGATGTATCGACAGCGCTGCCCTTGTGACTGTCTA 960
Db 300 HisTrpValThrThrTrpPheLeuLeuAspValIleAlaIleAlaLeuProPheAspLeu 319
QY 961 CATGCTTCAAGTCAAGGTACTTGTGGGGCCCATGTGCTGAGAGAGGCTGCTGTCTG 1020
Db 320 HisAlaPheLeuValAsnValTrpPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 339
QY 1021 GCGCTGTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Db 340 ArgLeuLeuArgLeuLeuProArgLeuAspArgGlySerGlnTrpSerAlaValValLeu 359
QY 1081 AACTGCTCATGGCGCTGTGCGCTGCTGCGACATGGGCTGCGCTGCTGCTTTC 1140

```

|||||  
Db 360 ThrLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 379  
OY 1141 ATTGCCAGCGGAGATGCAGAGACGCAATCCGAGTCCCTGAGATTGGCTGGCTGCAG 1200  
Db 380 IleGlyGlnArgGluIleGlnSerSerGlnSerGlnLeuProGluIleGlyTrpLeuGln 399  
OY 1201 GAGTGGCCCGCGAGTGGAGACTCCCTACTACTGCTGGTGGCCGAGGCGCACTGGAGG 1260  
Db 400 GluLeuAlaArgGlnLeuGlnTrpProTyrTyrLeuValGlyArgArgProAlaGlyGly 419  
OY 1261 AACAGCTCCGGCCAGAGTACAACTGCAGACAGCAGCAGGAGGCCAACCGGGGCGCTG 1320  
Db 420 AaaSerSerGlyGlnSerAspAsnCySerSerSerGlnAlaAsnGlyTrpGlyLeu 439  
OY 1321 GAGCTGCTGGGGGCGCGCTGGCGCAGCGGCTACATCACTCCCTACTCTGAGCTC 1380  
Db 440 GluLeuGlnGlyLysProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 459  
OY 1381 AGCAGCTCAGCAGGCTGGGCTTCGGCAACGTGTCGCCCAACAGCAGCAGCAGAGATC 1440  
Db 460 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLys 479  
OY 1441 TTCTCCATCTGCACCATGCTCATCGGCGCCGTGATGCACGCGGTGTGTTGGAACTG 1500  
Db 480 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal 499  
OY 1501 ACGGCATATCATCCAGCGATGTAACGCCCGCTTCTGTACCAACAGCGCAGCGCGAC 1560  
Db 500 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 519  
OY 1561 CTGCGGATCATCTCCGATCCACCGTATCCCAAGCCCTCAAGAGCGCATGTGGAG 1620  
Db 520 GlnArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGln 539  
OY 1621 TACTTCAGGCGCACTGGGCGGTGAACAATGAGCATGCAGACACCAACGAGCTGTGCAGAGC 1680  
Db 540 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 559  
OY 1681 CTCCTGACAGCTGGCGCGAGACATCGCATGCAGCTGCACAGAGAGGTCTGCAGCTG 1740  
Db 560 LeuProAspIleuLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 579  
OY 1741 CCACTGTTGAGCGCGCGCAGCGCGGCTGCTGCGGCGCATGTCTGCGCCCTGCGGCCC 1800  
Db 580 ProLeuPheGlnAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 599  
OY 1801 GCCTTCGCACGCGCGCGAGTACTCATCCACCAAGCGCATGCCGCGAGGCGCTTAC 1860  
Db 600 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 619  
OY 1861 TTGTGCTGCTGGCTCATGAGAGTGTCAAGAGTGGACCGCTGCTGCGCATCTAGG 1920  
Db 620 PheValLysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 639  
OY 1921 AAGGCGACCTGATCGCTGTGAGCTGCCCGCGGAGAGCAGGTGTAAAGGCCAATGCC 1980  
Db 640 LysGlyLysPheLeuIleGlyCysGluLeuProArgArgGlnGlnValValLysAlaAsnAla 659  
OY 1981 GAGCTGAGGGGTGAGCTACTGCTGCTGCAGTGTCTGACAGCTGGCTGGCTGCAGAGC 2040  
Db 660 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 679  
OY 2041 AGCTTGGCTGATCCCGAGATTGGCCCGGCTTCAGTCTGGCTGGCTGGCGGGAGCTC 2100  
Db 680 SerLeuAlaLeuTyrProGlnPheAlaProArgPheSerArgGlyLeuArgGlyLeuLeu 699  
OY 2101 AGCTAACACCGGGGTGGGGGAGGCTGCTGAGAGTGGAGCAGCAGCTCCCTAGCGGC 2160  
Db 700 SerTyrAsnLeuGlyAlaGlyGlySerAlaGlnValAspThrSerSerLeuSerGly 719  
OY 2161 GACAATACCTTATGTCCAGCTGAGAGAGAGAGACAGATGGGAGACAGGCGCCACG 2220  
|||||

Db 720 AspAsnThrLeuMetSerThrLeuGlnGluLysGluThrAspGlyGlnGlnLysProThr 739  
OY 2221 GCTCCCCAGCCCGACGCTATGAGCCCTCCAGCCCGCTGCTGCCCTGGCTGCACCTCC 2280  
Db 740 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProLysThrSer 759  
OY 2281 TCATCTCAGCTGCCAAGTGTGATCCCAAGCTGCAGAACAGCAGCCCGGCTGCTAGGT 2340  
Db 760 SerSerSerAlaAlaLysLeuLeuSerProArgGlyThrAlaProArgProArgLeuGly 779  
OY 2341 GGCAGAGGAGGCGCAGCAGGCGCAGGCGCTTGAAGCTGAGAGCTGAGGCTGCTGCTCC 2400  
Db 780 GlyArgGlyArgProGlyLysArgAlaGlyAlaLeuLysAlaGlyAlaGlyProSerAlaPro 799  
OY 2401 CCAAGGCGCTTGAAGGCTACGCGCTGCCCGCCATCCATGGAATGTGCCCGCAATCTG 2460  
Db 800 ProArgAlaLeuGlnGluLysLeuArgLeuProPheProTyrAspValProProAspLeu 819  
OY 2461 AGCCCGAGGTAATGATGGCATGAAAGCGGTGTGGCTGGAGCAGCAGCCAGTCTCT 2520  
Db 820 SerProArgValAlaAspGlyIleGlnAspGlyCysGlySerAspGlnProLysPheSer 839  
OY 2521 TTCGCGTGGCGCAGTCTGGCCCGAATGTAGCAGCAGCCCTCCCTGGACAGAGAGC 2580  
Db 840 PheArgValGlyLysSerGlyProGluCysSerSerSerProSerProGlyProGluSer 859  
OY 2581 GGCCTGCTCACTGTCCCATGGGCGCCAGCGAGCAGAGCAAGAACACACACTGACACAG 2640  
Db 860 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 879  
OY 2641 CTTCGCGAGCGGTGACAGAGCTGTACAGACAGGTGTCTGCATGCGGGAGAGACTGACAG 2700  
Db 880 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 899  
OY 2701 TCACCTGCCAGGCTGTGACAGCTTGTCCCTGGCGCCCAACAGGAGGAGGCTCGTCCCG 2760  
Db 900 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGlyGluProCysProArg 919  
OY 2761 GCATCGGAGAGGCGCGCGCCAGCAGCAGCTCCGCGGCTTGCAGCTCTGTGTGTG 2820  
Db 920 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 939  
OY 2821 GACACTGGGCACTCTCTCTGCTGCTGACAGCCCGCAGCTGCTGTGAGTGGAGT 2880  
Db 940 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 959  
OY 2881 TGGCCCAACCTGTCCGGGCGCTCTCCCTCATGGCACCTTGCGCTGGGCTGCCCA 2940  
Db 960 TrpProHisProArgProGlyProProProLeuMetAlaProArgProTyrGlyProPro 979  
OY 2941 GCGTCTCAGAGCTCCCTGCGCTGCAGCCACACACTTCTGGAGCTCACTCACTGAGCTCA 3000  
Db 980 AlaSerGlnSerSerProTyrProArgAlaThrAlaPheThrPheThrSerAspSer 999  
OY 3001 GAGCCCGCTGCTCAGAGGACTCTGCTGTGAGCCAGCAGCCCTGCTCCCTCTCTCT 3060  
Db 1000 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1019  
OY 3061 TCTGAGAGAGGAGCTAGAGTGGCGCGCAGAGCTGTGAGCCAGCTGAGCTGAGCTAGCAGC 3120  
Db 1020 SerGluGlnGlyAlaArgGlyGlyProAlaGluProValSerGlnAlaGlyAlaThrSer 1039  
OY 3121 ACTGAGAGCCCGCAGCAGGCTCAGGGGCGCTGGCGCTTGGCTGGAGCCCGCAGAGCTG 3180  
Db 1040 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTyrAspProHisSerLeu 1059  
OY 3181 GAGATGCTGTTATTGGCTGCAGAGCTGTGCAGACAGTCCAGTGCAGCAGCAGAGAGAGC 3240  
Db 1060 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGlnGlnGly 1079  
OY 3241 ACAGGCGTC 3249  
Db 1080 ThrGlyVal 1082  
|||||



## RESULT 4

US-09-600-776-6

Sequence 6, Application US/09600776

Patent No. 6326168

GENERAL INFORMATION:

APPLICANT: Yamamouchi Pharmaceutical Co., Ltd.

TITLE OF INVENTION: A novel potassium channel protein

FILE REFERENCE: Y9903-PCR

CURRENT APPLICATION NUMBER: US/09/600,776

CURRENT FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: JP P1998-011434

PRIOR FILING DATE: 1998-01-23

PRIOR APPLICATION NUMBER: JP P1998-346198

PRIOR FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6

LENGTH: 1017

TYPE: PRT

ORGANISM: Homo sapiens

US-09-600-776-6

Alignment Scores:

Pred. No.:	1,13e-153	Length:	1017
Score:	2461.50	Matches:	538
Percent Similarity:	59.19%	Conservative:	119
Best Local Similarity:	48.47%	Mismatches:	245
Query Match:	40.43%	Indels:	208
		Gaps:	23

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-600-776-6 (1-1017)

```

QY 1 ATGCCGGGAGTGGGGCTCTGGGGCTGAGAACGCTTCTGGACCACTGCTGAC 60
Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTGCAGCGGACGACAGTAATCTGCTGGGCGCAAGCGCCAGATGGCGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyThrArgGlyPhe 40
QY 121 CCCGGGCTCTACGCTGTGATGGCTGTGTGACCTGACGGGCTCTCCGGGCTAGATC 180
Db 41 ProIleValTyrCysSerAspGlyPheCysGlnLeuThrGlyTyrGlyArgThrGlyVal 60
QY 181 ATGAGCGGGGCTGCTGCTCTCTCTCTTATGGGCGACAGCACAGTGAAGCTGTCCGC 240
Db 61 MetGlnLysThrCysSerCysArgPheLeuTyrGlyProGlnThrSerGlnProAlaLeu 80
QY 241 CACAGATCCGACGAGGCTGAGGAGGACAGCAAGGTTCAAGGCTGACCTGATCTGAC 300
Db 81 GlnArgLeuHisLysAlaLeuGlnGlyHisGlnGlnHisAlaGlyAlaGlnIleCysPheTyr 100
QY 301 CGGAGAGCGGGCTCCCTTCTGTGTCTCTGATGTGATGATACCAATGAAGAGAGAA 360
Db 101 ArgLysAspGlySerAlaPheThrCysLeuLeuAspMetProIleLysAsnIleMet 120
QY 361 GGGAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 121 GlnIleValValLeuPheLeuPheSerPheLysAspIleThrGlnSerGlySerProGly 140
QY 421 ---GGCCCGGACAGATGAGAGAGACAGAGTGGCGCGCGCGCATAGGCCGGGACAGA 477
Db 141 LeuLysProGln-----GlyGlyArgGlyLysPheSerAsnHisGlnAsn 154
QY 478 TCCAAAGGC-----TTCATGCGCAACCGGCGCGGAGCGCGGCGG 516
Db 155 SerLeuGlnArgGlyAlaThrTrpLysPheArgSerAlaArgArgSerArgThr 174
QY 517 GTGCTTACCACTGTCTCCGGGACCTGACAGAGAGCGCCAGGAGGAGGAGGAGGAGGAG 576
Db 175 ValLeuHisArgLeuThrGlnHisPheGlyArgArgGlyGlnGlyMetLysAlaAsn 194

```

```

QY 577 AAGGGGCTTTTGGGAGAAACCAACTGCTGTGATCAAAAGTAGCCGCATCCGGAG 636
Db 195 AsnAsnValPheGlnProLysProSerValProGlnTyrLysValAlaSerValGly 214
QY 637 TCGCCCTTACCTGCTGTGACCTGTGGGACCTGAGACCACTGGGAGGCTTACCTG 696
Db 215 SerArgCysLeuLeuHisLysTyrSerValSerLysAlaIleThrPheAspGlyLeu 234
QY 697 CTCGCCACACTATGTGGGTGACAGTGGCCGACAGCGCTGTGTGACACAGCAGCG 756
Db 235 LeuAlaThrPheTyrValAlaValThrValProTyrAsnValCysPheSerGlyAsp 254
QY 757 GAGCCAGTGCCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 816
Db 255 AspThrProIleThrSerAlaGlnHisThrLeuValSerAspIleAlaValGlnMet 274
QY 817 ATCCTTGACATTTGTGTAATTTCCGTACCAATTCGTGTCAAGTCCGAGGAGGAG 876
Db 275 IleLeuAspIleIleLeuAsnPheArgThrThrTyrValSerGlnSerGlyGlnVal 294
QY 877 TTTGGCCCAAGTCCATTTGCTCCATGCTGACAGCACTGTGTCTGTGATGTCATC 936
Db 295 SerAlaProArgSerIleGlyLeuHisTyrLeuAlaThrPhePheIleAspLeu 314
QY 937 GCAGCGCTGCTGTGACCTGTACATGCTGACAGCTGACAGCTGACAGCTGACAGCT 996
Db 315 AlaAlaLeuProPheAspLeuLeuTyrIlePheAsnIleThrValThrSerLeuVal 334
QY 997 CTGCTGAGAGACGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056
Db 335 LeuLeuLysThrValArgLeuLeuAlaGlyLeuAlaTyrLeuLeuGlnAlaArgTyr 354
QY 1057 TGCAGTACAGCGCGCTGTGCTGACATGCTGATGCGGCTGTCCGCTGCTGCGGAC 1116
Db 355 SerGlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAla 374
QY 1117 TGGGTGCTGCTGCTGCTGCTGCTTACATGCTGACAGCGGAGATGAGAGAGAG 1176
Db 375 TrpMetAlaCysIleThrPyrValIleGlyArgArgGlnMetGlnAlaAsnProLeu 394
QY 1177 CTGCTGAGATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1236
Db 395 LeuThrAspIleGlyTyrPheHisGlnLeuGlyLysArgLeuGlnValProTyr 412
QY 1237 GTGGCGCGGAGCGACAGTGTGAGGAGAACAGCTCCGGCGAAGTGAACAATG 1296
Db 412 ----- 412
QY 1297 AGCGAGGCCAACGGGACGGGGCTGAGCTGTGGCGCGCGCGCTGCTGCGAGCGCTAC 1356
Db 413 -----ValAsnGlySer-----ValGlyGlyProSerArgArgSerAlaTyr 426
QY 1357 ATCAGCTCCCTTACTTGTGACACTGACAGACCTGACAGCGTGGGCTTGGCAAGCT 1416
Db 427 IleAlaIleLeuTyrPheThrLeuSerSerLeuThrSerValGlyPheLysAsnVal 446
QY 1417 GCCACAGGAGACAGGAGAGATCTTCTCACTGCTGACAGCTGATGAGCGGCTGATG 1476
Db 447 AlaAsnThrAspAlaGlnLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet 466
QY 1477 CAGCGGTGTGTGGGAGAGCTGAGGCGCATCAACGCGGATGAGCGCGCGGCTTT 1536
Db 467 HisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMetLysSerArgArg 486
QY 1537 CTGTACACAGCGCGACCTGCGGACCTGACATCCGATCCAGCTGATCCAG 1596
Db 487 LeuTyrHisSerArgMetLysAspLeuLysAspPheIleArgValHisArgLeuProArg 506
QY 1597 CCCCTCAAGCAGCGCATGCTGAGTACTTCCAGGCGACCTGCGCGGCTGAGAAATGCTATC 1656
Db 507 ProLeuLysGlnArgMetLeuGlnTyrPheGlnThrThrTrpAlaValAlaSerGlyIle 526
QY 1657 GACACCCAGGAGCTGCTGACAGAGCTCCCTGACAGAGCTGCGCGGACAGACATGCG 1716

```





US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-343-494-9 (1-1284)

QY 1 ATGGCGGCGCATGGGGGCTCTGGCGCTCAGAACACCTTCTGACACCATCGCTACG 60  
Db 1 MetProAlaArgLysGlyLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCAGCGGCGCGACAGTAACTTCTGCTGGGCAAGCCCGAGGGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAspValLeuLysAsnGlnAlaAsnGly--Asn 39  
QY 121 CCCGGTCTACTGCTCTGATGCTTCTGACCTCAGCGGCTTCTCCCGGCTGAGCTC 180  
Db 40 ProIleValIyrCysSerAspGlyPheValAspLeuThrIlyTrpSerArgAlaGlnIle 59  
QY 181 ATGCACCGGGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Db 60 MetGlnLysGlyCysSerCysHisPheLeuTyrGlyProAspThrLysGlnGlnHisLys 79  
QY 241 CAACACATCCGACAGCCCTGACAGACACAGAGTCAAGGCTGAGCTGATCTGTAC 300  
Db 80 GlnGlnIleGlnLysSerLeuSerAsnLysMetGlnLeuLysLeuGlnValIlePheTyr 99  
QY 301 CGAAGACGGGGCTCCGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
Db 100 LysLysGlnGlyAlaProPheTyrCysLeuPheAspIleValProIleLysAsnGlnLys 119  
QY 361 GGGAGGAGGCT 411  
Db 120 ArgAspValValLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGln 139  
QY 411 ----- 411  
Db 140 MetAsnValAsnGlnGlnLysAspSerValPheAlaLeuThrAlaAlaLeuGlnIlyAla 159  
QY 412 -----AACGAGGG 420  
Db 160 ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyGlyLeuProGlnLeuGly 179  
QY 421 GGGCCC-----GACAGATGAGAGAGAGACAGTGGGGCGCGCGCATATGGCCGG 471  
Db 180 GlyProAlaAlaSerAspGlyAspThrGlnAlaGlnGlyGlnGlyAsnAsnLeuAspValPro 199  
QY 472 GCACGATCCAAAGGCTTCAATGCACAACCGCGCGGAGCGCGCGCTGCTCTACCACTG 531  
Db 200 Ala-----GlyCysAsnMetLysArgArgSerArgAlaValLeuTyrGlnLeu 216  
QY 532 TCCGGGACCTGACAGAACGCCCAAGGAGC--AAGCACAGGCTCAATAAGGG-- 582  
Db 217 SerGlnHisTyrLysProGlnLysGlyValLysThrLysLeuLysLeuGlyAsnAsn 236  
QY 583 ---GTGTTGGGGAGAAACCAACTTGCTGCTAGTACAAGTAAAGCGCCATCCGAGAGTCG 639  
Db 237 PheMetHisSerThrGlnAlaProPheProGlnLysThrLysGlnSerIleLysLysSer 256  
QY 640 CCTTCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699  
Db 257 ArgLeuLeuLeuProHisTyrGlyValPheLysGlyIleTrpAspTrpValIleLeuVal 276  
QY 700 GCCACACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759  
Db 277 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAspArg 296  
QY 760 CCCAGTCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTATC 819  
Db 297 GlnThr-----LysValSerAspValIleValGlnAlaLeuPheIle 310  
QY 820 CTTCGACATTGTGCTGAATTCCTGACACATTCCTGCTGCTGCTGCTGCTGCTGCT 879  
Db 311 ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlnValValSer 330  
QY 880 GCGCCAAAGTCATTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939  
Db 331 AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTrpPheAlaLeuAspLeuAla 350

QY 940 GCGGTCGCTTTCGACCTGCTATGCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCA 990  
Db 351 AlaLeuProPheAsp-----HisLeuTyrAlaSerAspLeuTyrAspGlyLysAspSer 368  
QY 991 ---GCCCTGCTGTAAGAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047  
Db 369 HisIleHisLeuValLysLeuThrArgLeuLeuThrGlnAlaArgLeuLeuGlnLysIle 388  
QY 1048 GACCGGATCTGACATGACAGCGCGGTGCTGACACTGTCATGAGCGCGCTTGGCCCTG 1107  
Db 389 AspArgTyrSerGlnHisThrAlaMetIleLeuThrLeuLeuMetPheSerPheThrLeu 408  
QY 1108 CTGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1167  
Db 409 AlaIleHisTyrLeuAlaCysIleTrpTyrValIleAlaValLysGlnTyrGln----- 426  
QY 1168 GAATCCGAGCTGCTGAG-----ATTGGCTGCTGACAGAGCTGCGCCGCGACTGAG 1221  
Db 427 -----TrpPheProGlnSerAsnIleGlyTrpLeuGlnLeuLeuAlaGlnArg----- 442  
QY 1222 ACTCCCTACTACTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1281  
Db 442 ----- 442  
QY 1282 AACTGACAGCAGACAGCGAGCGCAACGGAGCGGGCTGAGCTGCTGGCGCGCGCTCG 1341  
Db 443 -----LysAsnAlaSerValAlaIleLeuThrThrAlaIle----- 454  
QY 1342 CTGCGGAGCGCGCTACATACCTCCCTCTACTTCTGCTGCTGCTGCTGCTGCTGCT 1401  
Db 455 -----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerLeuThrSerValGly 471  
QY 1402 TTGCGGACGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1461  
Db 472 PheGlyAsnValSerHisAsnThrThrAlaGlnLysValPheThrIleLeuMetLeu 491  
QY 1462 ATGCGCGCGCTGATGACGCGGGGCTGTTGGAACTGACGCGCGCATATCCAGCGCATG 1521  
Db 492 IleGlyAlaLeuMetHisAlaValAlaPheGlyAsnValThrAlaIleIleGlnArgMet 511  
QY 1522 TACGCGCGCGCTTCTGACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1581  
Db 512 TyrSerArgArgSerLeuTyrGlnLysLysTyrPheArgAspLeuLysAspPheValAlaLeu 531  
QY 1582 CACCGTATCCCAAGCGCCCTCAAGCAGCGCATGCTGAGTACTTCCAGGCGCACTGGGG 1641  
Db 532 HisAsnMetProLysGlnLeuLysGlnArgIleGlnAspTyrPheGlnThrSerTrpSer 551  
QY 1642 GTGAACAATGCGATGACACACAGCGAGCTGTCAGAGCGCTCTGACAGCGTGGCGCA 1701  
Db 552 LeuSerHisGlyIleAspIleTyrGlnThrLeuArgGlnPheProGlnLysLeuArgGly 571  
QY 1702 GACATGCGCATGACCTGACACAGAGAGTCTGCACTGCTGCACTGTTTGAAGCGCGCAGC 1761  
Db 572 AspValSerMetHisLeuHisArgGlnIleLeuGlnLeuProIlePheGlnAlaIleSer 591  
QY 1762 CGCGGCTCTGCGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1821  
Db 592 GlnGlyCysLeuLysLeuLeuSerLeuHisIleLysThrAsnPheCysAlaProGlnGln 611  
QY 1822 TACCTCATCCACAGCGAGCGCTGAGCGCGCTCTACTTTCCTGCTGCTGCTGCTGCT 1881  
Db 612 TyrLeuIleHisLysGlyAspAlaLeuAsnTyrIleTyrTyrLeuCysAsnGlySerMet 631  
QY 1882 GAGTGTCAAAGGTGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1941  
Db 632 GlnValIleLysAspAspMetValValAlaIleLeuGlnLysGlyAspLeuValGlySer 651  
QY 1942 GAGCTG----- 1947  
Db 652 AspIleAsnValHisLeuValAlaThrSerAsnGlnGlnMetThrAlaThrThrAsnSer 671





```
OY 2143 ACCAGCTCCCTGAGGGGAGACAAATACCTTATGTCACGCTGGAGAGACAGACACT 2202
      |||||
DB 879 GtlypHeserArglnArglySerPheArgArgThrAsp 898
OY 2203 GGGAGACAGGGCCCAAGCTCTCCCAAGCTGAGAGACCTCCAGCCCTGCTG 2262
      |||||
DB 899 ThrGln 901
OY 2263 TCCCTGGTGGACCTCATCTCAGTGCACAGCTGTATCCCACTGACAGACGA 2322
      |||||
DB 902 ---ProGlyGlnValSerAla 914
      |||||
OY 2323 CCCCAGCTGCTGTAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2382
      |||||
DB 915 AlaGlyPro 932
      |||||
OY 2383 GCTGGCCCTGCTGCTCCCA 2418
      |||||
DB 933 SerGlyProSerSerProGlnSerSerGlnAspGlnGlyProGlnArgSerSerPro 952
      |||||
OY 2419 CTACGGCTG 2466
      |||||
DB 953 LeuArgLeuValProPheSerSerProArgProGlnGlyGlnGlyPro 972
      |||||
OY 2467 AGGCTAGTATGAGCATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2514
      |||||
DB 973 ---LeuMetGlnAspCysGlnSerSerAspThrCysAsnProLeuSerGlnAlaPhe 991
      |||||
OY 2515 ---TTCCTCTTC 2538
      |||||
DB 992 SerGlyValSerAsnIlePheSerPheThrProGlnAspSerArgArgGlnGlnGln 1011
      |||||
OY 2539 GGGCCGGAATGTAAGACAGACAGCCCTCCCTGACACAGAGAGAGAGAGAGAG 2555
      |||||
DB 1012 LeuProArgGly 1026
      |||||
OY 2596 ---CCCATGGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2634
      |||||
DB 1027 LeuSerSerProGlnArgArgProArgGlnAspValIleSerArg 1042
      |||||
OY 2635 GACAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2691
      |||||
DB 1043 AspAlaLeuGlnArgGlnLeuAsnArgLeuGlnThrArgLeuSerAlaAspMetAlaThr 1062
      |||||
OY 2692 GAGCTGACATCTCGCCAGAGCTGTGACAGCTGTCTGCGGCCCAAGAGAGAGCTCG 2751
      |||||
DB 1063 ValLeuGlnLeuGlnArgGlnMetThrLeu 1073
      |||||
OY 2752 TGCCCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2811
      |||||
DB 1074 ---ValProAlaThrSerAla 1080
      |||||
OY 2812 CTGTGTGTGACACTGGGAGACTCTCTACTGCTGACAGAGAGAGAGAGAGAGAG 2871
      |||||
DB 1081 ---ValThrThrProGlnProGlnProGlnProGlnProGlnProGlnProGln 1099
      |||||
OY 2872 AGTGGAGACTGGCCCAAGCTCTGCGGGGCTCTCCCTCATGAGAGAGAGAGAGAG 2931
      |||||
DB 1099 OLeu 1110
      |||||
OY 2932 GGTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2982
      |||||
DB 1111 -ValSerIlePheMetAlaCysGlnGlnLeuProProGln 1129
      |||||
OY 2983 ACCTCAGCTGAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3042
      |||||
DB 1129 nglIuGlyProThrArgArgLeuSerLeuProGlnGlnGlnGlnGlnGlnGln 1149
      |||||
OY 3043 CCGT 3046
      |||||
DB 1149 OLeu 1150
      |||||
```

```
RESULT 7
US-09-351-215-13
Sequence 13, Application US/09351215
Patent No. 6087488
GENERAL INFORMATION:
APPLICANT: Genetec, Barry S.
APPLICANT: Titus, Steven A.
TITLE OF INVENTION: Polynucleotides Encoding Herg-3
FILE REFERENCE: 960296, 94550
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 08/956,242
EARLIER FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 13
LENGTH: 1159
TYPE: PRT
ORGANISM: Homo sapien
US-09-351-215-13

Alignment Scores:
Pred. No.: 5, 93e-94
Score: 1551.00
Percent Similarity: 44.86%
Best Local Similarity: 33.54%
Query Match: 25.47%
DB: 3
Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-351-215-13 (1-1159)

OY 1 ATGCGGCGCATGCGGGGCTCTGCGGCTGACAGACACTTCTGAGACACCTGCTACG 60
      |||||
DB 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleAlaArg 20
      |||||
OY 61 CGCTTCACGGCAGACAGACAGAACTTGTGCTGGAGAGAGAGAGAGAGAGAGAGAG 120
      |||||
DB 21 LysPheGlnGlnSerArgLysPheIleAlaAsnAlaArgValGlnAsnCys 39
      |||||
OY 121 CCCGTGCTACTGCTGATGAGCTTGTGACCTCAAGAGAGAGAGAGAGAGAGAGAG 180
      |||||
DB 40 AlaValIleThrCysAsnAspGlyPheCysGlnLeuGlySerArgAlaGlnVal 59
      |||||
OY 181 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
      |||||
DB 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
      |||||
OY 241 CAACAGATCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
      |||||
DB 80 AlaGlnIleAlaGlnAlaLeuLeuGlnGlyAlaGlnGlnGlyValGlnIleAlaPheThr 99
      |||||
OY 301 CGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
      |||||
DB 100 ArgLysAspGlySerCysPheLeuGlyLeuValAspValAlaProValHisGlnAsp 119
      |||||
OY 361 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
      |||||
DB 120 GlnAlaValIleMetPheIleLeuAsnPheGlnValIleMetGlnLysAspMetValGly 139
      |||||
OY 400 ---AGCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
      |||||
DB 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerThrPheLeuAlaProGlnArg 159
      |||||
OY 435 --- 435
      |||||
DB 160 AlaLysThrPheArgLeuLysLeuProAlaLeuAlaLeuThrAlaArgGlnSerSer 179
      |||||
OY 436 ---AAGAGACAGAGTGTGTGCGCGCGGATGTGCGCGGCG---ACGATCCAAAGCTTC 489
      |||||
DB 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlnLysAlaValAlaAspValAla 199
      |||||
OY 490 AATGCCACCGGCG 503
      |||||
```







Db 219 sPasnHisValAlaGluLeuGlyProAlaGluValArgAlaLeuValGlyProGly 239  
QY 525 ---CAACSTGTCCGGCACTGCAAGACGCCCAAGGCAAG---CAACAAGCTCAAT--- 576  
Db 239 ePProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258  
QY 576 ----- 576  
Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGlySerCysAlaSer 278  
QY 577 -----AAGGGGGTGTGGGAG 594  
Db 279 ValArgArgAlaSerSerAlaAspAlaSerProGlyAlaMetArgAlaGlyValLeuProPro 298  
QY 595 AAACCAAC----- 603  
Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318  
QY 603 ----- 603  
Db 319 ThrSerAspSerAspLeuValArgThrArgThrIleSerIleIleProGlnIleThrLeu 338  
QY 603 ----- 603  
Db 339 AsnPheValAspLeuGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358  
QY 603 ----- 603  
Db 359 IleAlaProGlyIleLeuGlyAlaArgThrHisAsnValThrGlyLeuValThrGlnValLeu 378  
QY 604 -----TTGCCTGAGTACAAAGTACGCCATCCGAGAGGCGCCTTC 645  
Db 379 SerLeuGlyAlaAspValLeuProGlyIleArgIleGlnAlaProArgIleHisArgThr 398  
QY 646 ATCCTGTGCACSTGTGGGCACTGAGACACACCTGGAGTGCCTTCATCCTGCTGCCACA 705  
Db 399 ThrIleLeuHisIleArgSerProPheLeuAlaValTrpAspTrpLeuIleLeuLeuVal 418  
QY 706 CTCTATGAGCTGCACAGTGCCTACAGCCTGTGTG-----AGCACAGCACGG 756  
Db 419 IleThrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuGlyGlnIleGlu 438  
QY 757 GAGCCAGTGC-----GCCCGGCGCCGCCAGCGGTGGTACCTGGCC 801  
Db 439 GlyProProAlaThrGlyCysGlyTyrAlaCysGlnProLeuAlaValAlaAspLeuIle 458  
QY 802 GTGAGAGCTCCTTCATCCTTACATTCGTGATTCGTAATTCCTTACACATTCGTGCTCAAG 861  
Db 459 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsnAla 478  
QY 862 TCGGGCAAGCTGTGTTGCCCAAGTCCATTCGCTCCACATCAGTACACACCTGCTGTC 921  
Db 479 AsnGlnIleValAlaSerHisProGlyArgIleAlaValHisTyrPheLeuGlyTrpPhe 498  
QY 922 CTGCTGATGTCATCCGAGAGCTCCCTTCGATTCGCTGATTCGCTTCACAGCTCAAGCTG 981  
Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeu----- 511  
QY 982 TACTCGGGGCT-----CATCTGTGAAGAGGCTCCGCTGCTGCTG 1023  
Db 512 IlePheIleSerGlySerGlyGlnLeuIleGlyLeuLeuIleIleAlaGlyLeuValArg 531  
QY 1024 CTGCTGCGCTGCTCCGCGCTGACCGGCTACCTGACGAGTACAGCGCGGTGCTGACA 1083  
Db 532 LeuValArgValAlaArgGlyLeuAspArgTyrSerIleTyrGlyAlaAlaValLeuPhe 551  
QY 1084 CTGCTATAGGCGCTGCTCCGCTGCTGCGCACCTGAGTGCCTGCTGCTGCTTATCAT 1143  
Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisIleThrLeuAlaCysIleThrTyrAlaIle 571  
QY 1144 GCGCAGCGGAGATCGAGACAGCAATCCGACCTGCTGATGCTGCTGCTGCTGAGAG 1203  
Db 572 GlyAsnMetGlnIleProHisMetAspSer-----ArgIleGlyTrpLeuHisAsn 588

QY 1204 CTGCGCGCGCACTGAGACCTCCCTACTACTGCTGCTGCGCGGAGCCAGCTGAGGAGAC 1263  
Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598  
QY 1264 AGCTCCGCGAGAGTACAACTGACACAGACAGCAGAGGCCAAAGGAGCGGGCTGAG 1323  
Db 599 SerSerGly----- 601  
QY 1324 CTGCTGCGCGCGCGCTGCTGCGCACGCTCATCATCCTCCTTACTGCACTGAC 1383  
Db 602 ---LeuGlyGlyProSerIleLeuAspIleGlyValThrAlaLeuIleThrPheSer 620  
QY 1384 AGCCTACACAGGCTGGGCTTCCGCAACGCTGCCCAACAGCGACACCGAAGATCTTC 1443  
Db 621 SerLeuThrSerValGlyPheGlyAsnValSerProAspThrAsnSerGlyLysIlePhe 640  
QY 1444 TCCATCTGCACATGCTCATCGGCGCTGATGACAGCGGCTGTTGGGAACGTGAG 1503  
Db 641 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer 660  
QY 1504 GCATCATCCACAGCATGATGACCCGCGCTTGTCTGTACACAGCCGACGCGGCACTG 1563  
Db 661 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680  
QY 1564 CGCGACTATATCCGATCCACCGATATCCCAAGCCCTCAAGACAGCGCATGCTGAGTAC 1623  
Db 681 ArgGlnPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlnIleTyr 700  
QY 1624 TTCACGGGCACTGGCGGCTGAAACAATGGCATGCAACACCGAGCTGCTGCAAGACTC 1683  
Db 701 PheGlnHisAlaIleTyrSerIleThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 720  
QY 1684 CCTGACGAGCTCGCGGACATCGCATGCACTGCAACAGAGGTCTGTGAG---CTG 1740  
Db 721 ProGlnCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuGlnHisCys 740  
QY 1741 CCATGTTTGAAGCGGCAAGCGCGCTGCTGCGGCACTGCTGCTGCGCGGCGCC 1800  
Db 741 LysProPheArgGlyAlaThrIleLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760  
QY 1801 GCCTTCTGACGCGCGGCGAGTACCTCATCCACAGCGGATCCCTGACGCGCTTAC 1860  
Db 761 ThrHisAlaProProGlyAspThrLeuValHisIleGlnAlaAspLeuIleThrAlaLeuTyr 780  
QY 1861 TTTGCTGCTGCTGCTCATGAGGTGCTCAAGGTGCGCACCGCTGCTGCCATCTTAC 1920  
Db 781 PheIleSerArgGlySerIleGlnIleLeuArgGlyAspValAlaIleIleGln 800  
QY 1921 AAGGCGACCTGATCGGCTGTGAGCTGCCCGCGGCGGAGCAAGTGTAAAGCCAAATGCC 1980  
Db 801 LysAsnAspIlePheGlyGlnProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820  
QY 1981 GACGTGAAGGCTGACCTACTGCTGCTGCAAGTGTGCAAGTGTGCTGGCTGAGTACAGAC 2040  
Db 821 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuIle 840  
QY 2041 AGCCTTGGCTGTACCCCGAGTTTGCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100  
Db 841 ValLeuAspMetTyrProGlnPheSerAspHisPheTrpSerLeu-----GluIle 858  
QY 2101 AGCTACAACTG-----GTCCTGGGAGAGCTCTGACAGAGTGCAC 2142  
Db 859 ThrPheAsnIleValArgAspThrAsnMetIleProGlySerProGlySerThrGlnLeuGln 878  
QY 2143 ACCAGCTCCCTGACGCGGAGCAATACCTTATGTCACGCTGGAGGAGAGAGACAGAT 2202  
Db 879 GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgThrAspLysAsp 898  
QY 2203 GGGAGCAGGAGGCCCAAGCTCTCCAGGCCCAAGCTGATGAGCCCTGACGCGCTGCTG 2262  
Db 899 ThrGlnIle----- 901

```

FILE REFERENCE: 2323-136
CURRENT APPLICATION NUMBER: US/09/226,012
CURRENT FILING DATE: 1999-01-06
EARLIER APPLICATION NUMBER: 09/122,847
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1159
TYPE: PRT
ORGANISM: Homo sapiens
US-09-226-012-4

Alignment Scores:
Pred. No.: 5.93e-94 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86% Conservative: 143
Best Local Similarity: 33.54% Mismatches: 337
Query Match: 25.47% Indels: 360
DB: 4 Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-226-012-4 (1-1159)
QY 1 ATGCCGGCCATGCGGGGCTCTGGCGCTCAGAACACTTCTGGACACCATCGCTACG 60
Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleIleArg 20
QY 61 CGCTTCAGCGGACGACGACAGTAACTTGTCTGTGGCAACCCGACCGGCGGGGCTCTTC 120
Db 21 LysPheGluGluGlnSerArgLysPheIleLeuAlaAsnAlaArgValGluAsnCys-- 39
QY 121 CCCGGGCTCTGTCTGTATGAGGCTTCGTATGACTCAAGGGCTCTCCGGGTGAGTTC 180
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerAlaGluVal 59
QY 181 ATGCAAGCGGGGCTGTGCTGCTCTCTCTCTCTTTATGGGCGACAGACCACTGAGCTGTCGC 240
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
QY 241 CAACAGATCCGACAGCCCTGACGACGACACAGAGTTCAAGGCTGAGCTGATCTGTAC 300
Db 80 AlaGlnIleAlaGlnAlaIleLeuGlnGlyAlaGluIleValGluIleAlaPheTyr 99
QY 301 CGGAAGACGGGCTCCCTTCTGTGCTCTCTGTATGATGATGATACCCATTAAGATGACAA 360
Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValAlaProValLysAsnGluAsp 119
QY 361 GGGGAGGGGCTCTCTCTCTCTA-----GTCCTCAACAGACATC----- 399
Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValAlaMetGluLysAspMetValGly 138
QY 400 -----AGCGAACCACAGACAGGAGGGGCCCCGACAGATGG----- 435
Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerThrPleuAlaProGlyArg 155
QY 435 ----- 435
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 177
QY 436 ---MAGGACACAGGTGGGCGCGCGCGCGGAGATATGGCCGGG---ACGATCCAAAGCTTC 488
Db 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValAlaValAspValAla 199
QY 490 AATGCCAACCGGCG----- 508
Db 199 splenThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMet 211
QY 504 -----GGGAGCGCGGCGGCTCTA----- 524
Db 219 spAsnHisValAlaGlyLeuGlyProAlaGluGluIleArgAlaLeuValGlyProGlyLys 233
QY 525 --CAACTCTCCGGGCACTTCAGAGAGACGCCCAAGGCAAG---CACAGCTCAT--- 576
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```







```

QY 2761 GC-----ATGGGAGAGGGGCCCGCCACGACGACC 2793
Db 769 lysergluryrglnaryprollelelglnleudetrgthrserglnproglnalaseri 789
QY 2794 TCGGGGT-----TCGACAGCCTGTGTGTGGAGACTGGGGCATCTCTAC 2841
Db 789 lelysrhapargserphaserprosserelncys-----801
QY 2842 TGCGTGACGCCCCAGCTGCCTGTCTTGAAGTAGGACATTGGCCCCACCCGTCGGGG 2901
Db 802 -----ProgluphelauspseuduluyserlyseulyserlysgluserL 818
QY 2902 CCTGCTCCCTCAGGACCCCTGGCCCTGGGGTCCCCACGCTCTAGAGCTCCCCCTGG 2966
Db 818 euserSerGlYAlHlsleuananThrAlaserGlunspasnleuthrserLeuleulg 838
QY 2962 CCTGAGCCCAAGCTTTCTGGACTCCACTCAGCTCAGACTGAGGCCCCCTCAGAGAGC 3022
Db 838 lnasPeraSpLeusereudluheuhlsleuarvglnarqlysthrYVal---HSP 857
QY 3022 CTCGCTCTGAGCCGAGACCCCTGCCCCTCCCTCC 3059
Db 857 roile-----ArghIsProserieuProaspser 866

RESULT 11
US-09-351-215 -4
Sequence 4, Application US/09351215
Patent No. 6087488
GENERAL INFORMATION:
APPLICANT: Ganetzky, Barry S.
APPLICANT: Titus, Steven A.
TITLE OF INVENTION: Polynucleotides Encoding Hery-3
FILE REFERENCE: 960296.94550
CURRENT APPLICATION NUMBER: US/09/351.215
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 08/956.242
EARLIER FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 868
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: unsure
LOCATION: (133)
OTHER INFORMATION: Unidentified at time of filing
FEATURE:
NAME/KEY: unsure
LOCATION: (181)
OTHER INFORMATION: Unidentified at time of filing
FEATURE:
NAME/KEY: unsure
LOCATION: (438)
OTHER INFORMATION: Unidentified at time of filing
FEATURE:
NAME/KEY: unsure
LOCATION: (439)
OTHER INFORMATION: Unidentified at time of filing
FEATURE:
NAME/KEY: unsure
LOCATION: (567)
OTHER INFORMATION: Unidentified at time of filing
FEATURE:
NAME/KEY: unsure
LOCATION: (568)
OTHER INFORMATION: Unidentified at time of filing
FEATURE:
NAME/KEY: unsure
LOCATION: (571)
OTHER INFORMATION: Unidentified at time of filing
FEATURE:
NAME/KEY: unsure

```







```

? CURRENT FILING DATE: 1997-10-22.
? NUMBER OF SEQ ID NOS: 13
? SOFTWARE: Patentln Ver. 2.0
? SEQ ID NO 2
? LENGTH: 626
? TYPE: PRT
? ORGANISM: Homo sapien
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (44)..(542)
? OTHER INFORMATION: Unidentified at time of filing
US-08-956-242-2

```

Alignment Scores:	
Pred. No.:	6,04e-46
Score:	817.50
Percent Similarity:	58.80%
Best Local Similarity:	43.13%
Query Match:	13.43%
DB:	2
Length:	62
Matches:	17
Conservative:	65
Mismatches:	11
Indels:	60
Gaps:	10

US-09-965-830-1\_COPY\_b\_3257 (1-3252) X US-08-956-242-2 (1-626)

QY 498 CCGGCGGGGAGCGGGGCCGTCGTCACCAACCTGTCCGGGACACCTGCAG---AAGCAGCC 554  
 |||::||| ||| ||||| ||| |||  
 Db 56 ProSerAlaHisGlnSerArgGlyHisProPro-SerSerHisTyrThrPheProArgPr 75

QY	555	CAAGGGCAAGCACAAGCTCAATTAAGGGGCTG-----TTTGCGGA	593
Db	75	oGlnProSerArgProValSerProAlaLeuAlaIaProCysLeuThrSerLeuGlyPr	95

QY 594 GAACCAAC-----TTGCTGATGACAAAGTAGCCGCAT 6299  
|||  
|||  
Db 95 OHISProGlnValLeuSerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnIleApr 115

QY 630 CCGGAAGTGGCCCTTCATGCTGTGTGCACCTGGGGCACTGAGACCCACCTGGGATGGCTT 689  
||| ::::|  
Db 115 oargllehsargtgrphltleuhsistySerProhelayalavaltprAspstrtle 135

QY 690 CATCTGCTGGCAGACTATATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTGACAC 749  
 |||||  
 :||| ||||  
 Db 135 uileleuLeuLeuValIleTyrThrAlaValAlaPheThrProTvsSeraIaaIaphetaule 155

```

QY      750 AGCAGCGGAGCCCAgTGCcGccCGCGGC-----CCGCCAGCGT 788
      :::      ::| | | | |
Db      155 userApg[InApg[userArdArg[va]aCvsaSerTuvrCvsaScdrOfCumb-vt 177

```

[illegible]

849 ATTCTGTCGAAGTGGGCCAGGTGGTGTTTGCSCCAAGTCCATTTCCTCACAACGT 908  
|:::||||:: ::||| |::: |||  
195 TTTTATAsnThrAspAsnGlnValValSerHisProAlaLeuTyr \*  
|:::||||:: ::||| |::: |||

909 CACCACTGTTCTCTGGATGTCATCGCAGCGTCCCTTTGACCTGTA----- 960  
|||||:::|||||:::|||||:::|||||  
215 alvega|wrrrbob|out|-b-w-+w-13|}|||||

[illegible]

1017 GCTGGCCCTGCTGCGGCTGCTTCGCGGCTGGACCGGTACTTCGACATACAGCCCGGTGT 1076

1077 GCTGACACTGCTCAGAGGCCGTGTTGCGCCCTGCTCGCCGCACTGGGTGCGCCTGCGTCTGTTT 1136

273 LNEURHELEUWUEWCYSTHPHREALULELALAHISTPRLDUALCYSLLETPTLY 293  
1137 TTACATTGGCCAGCGGAGATCCGAGACGCGAATCCGACTGCCTGAGATTGGCTGGCT 1196

Db 293 rAlaIleGlyAsnValGluArgProTyrLeuGluHis-----LysIleGlyTyrLe 310

```
Db      310 uaspSerLeuAlaValGlnIleu-----GIYLSarqTYraSnGl   323
```

323 Y-----SerAspProlaser----- 328

131 GCTGAGGCTGCTGGGCGGCGGCTGCGTGGCGAGCGGCTACATACCTCCCTTACTTCG 137  
 |||||::: ||:::|||||  
 Db 329 -----GLYProSerValGlnAspLysTyrValThrAlaLeuTyrPheTh 343

QY 13// AC1CAGCAGCCTCACCAGCGTGGGCTTCGGCAACGTCCTCCGCCAACACAGGACACCGAGAA 143  
 |||||  
 Db 343 rPheserSerLeuthrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGlyIu 363

DQ 1437 GATCTTTCACATCGACCATTGCTATCGGGGCCCTCATGCACGGGTGTTCGGAA 1499  
:::||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 363 sValpheserIleCysvalmetLeuIleGlyserLeumetTyralaserIlePheGllys 383

DY	1497	CGTGACGGCCATCATTCACGCCGANTAGCCGCCGTTTCTGTACCACAGCCGCACGCG	155
		:::     :::   :::	
Dd	383	nvalserAlallelelncglnArgLeuTyrSerGlyThrlAlaArgTyrHisMetGlnMetIe	403
		:::	

DQ 1557 CGACCTGGCGACTAGATCCGATCCACGCTATCCCCAAGCCCTCAAGACGCCATCCT 1616  
 : : : : :  
 Db 403 uArgValIysGIuPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgTyrLeuGln 423

Qy 1617 GGAGTACTTCCAGGCCACCTGGGCGGTGACACATGGCATCGAC 1659  
 |||||  
 Db 423 uGUUTrPheGlnHisAlaTrPrHrTyTrAsnGVIeAsn 437  
 |||||

RESULT 13  
US-09-351-215-2  
: Sequence 2, Application US/09351215

```

; / talent NO.008/488
; GENERAL INFORMATION:
; /
; / APPLICANT: Ganetzky, Barry S.
; /
; / APPLICANT: Titus, Steven A
; /

```

FILE REFERENCE: 960296.94550  
TITLE OF INVENTION: Polynucleotides Encoding Herg-3  
CURRENT APPLICATION NUMBER: US/09/351,215  
CURRENT FILING DATE: 1000-07-13

EARLIER APPLICATION NUMBER: 08/956,242  
EARLIER FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 13  
SEQUENCE: Data not available

```

; SEQ ID NO 2
;
; LENGTH: 626
;
; TYPE: PRT
;
; ORIGIN: 1-626

```

```

FEATURE:
NAME/KEY: unsure
LOCATION: (441)..(542)

```

Alignment Scores:

Score:	626
Percent Similarity:	179
Best Local Similarity:	65
Best Local Similarity:	111
Conservative:	65
Mismatches:	111
Matches:	179
Length:	626
Score:	626
Percent Similarity:	179
Best Local Similarity:	65
Best Local Similarity:	111
Conservative:	65
Mismatches:	111
Matches:	179
Length:	626

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-351-215-2 (1-626)

498 CCGGGGGGAGCCCGCGCTGTACACACCTGTCCGGGACACTGCAG--AAGCAGCC 554  
 |||::||| ||| ||||| ||| ||| ::|||  
 56 ProSerAlaHisGlnSerArgGlyHisProPro-SerSerHisTyrThrPheProAlaGpr 75



```

Db      88  GlyAlaProGlyProAlaGly-----ProProGlySerArgGlyAsp--- 101
OY      231  GCTGCTCCGCCAACAAGATCCGACAGGCGCTTGACGACAGACAGAGATTCAAGCTGAGCT 290
Db      102  ProGlyProProGlyAlaPro---GlyProAlaGlyProProGlySerArgGly----- 118
OY      291  GATCCGTACCGGACAGAGCGGCTCCCGTTCGTCTCCGTGATGATGATACCATMAA 350
Db      119  AspProGlyPro-----ProGlyAlaPro----- 126
OY      351  GAATGAGAAAGGAGGTGCTCTCTCTAGTCTCTACACAGACATACGCAAAACCA 410
Db      127  -----GlyProAlaGlyProProGlySerArgGlyAspProGlyProPro 141
OY      411  GAACGAGGAGGCGCCGACAGATGAGAGAGACAGGTGTGGCGCGCGCGGATAGTGGCCG 470
Db      142  GlyAlaProGlyProAlaGlyProProGlySerArgGlyAspProGlyPro-----Pro 159
OY      471  GGCACGATCCAAAGGCTTCATGCCAACCGCGCGCGGACCGCGCGCTCTACCACT 530
Db      160  GlyAla---ProGlyProAlaGlyProProGlySerArgGlyAspProGlyProProGly 179
OY      531  GTCCGGGACCTGCGACAGAACGACCCCAAGGCGCAACAGTCATAGAGGGGTGTGG 590
Db      179  IapProGlyPro-----AlaGlyProProGlySerArgGlyAspProGly 193
OY      591  GGAGAAACCAACTGCTGAGTACAAAGTACCCGCAATCC----- 631
Db      193  Iy-----ProProGlyAlaProGlyProAlaGlyPro 203
OY      632  ----GGAAGTCCGCTTCATCTGTTGACTGTGGAGTGGGACAGACAGCCACTGGAGTGG 686
Db      203  roProGlySerArg-----GlyAspProGlyProProGlyAlaPro 216
OY      687  CTATCTCTGCTGCGACACTATATGTGCTGTCACTGTGCCCTACAGCGTGTGTGAG 746
Db      216  roGlyProAlaGlyProPro-----G 223
OY      747  CACAGACAGGAGAGCCAGTCCGCGCGCGCGCC---CGCCAGCGTGTGTGACCTGGC--- 800
Db      223  IySerArgGlyAspProGlyProProGlyAlaProGlyProAlaGlyPro---ProGlySer 242
OY      801  CGTGAGAGTCTCTTCAATCCCTGACATGTGTGTAATTCGGTACACATTCGTGTCCA 860
Db      243  ArgGlyAspPro----- 246
OY      861  GTCCGCGCAGGTGCTGTTGGCCCAAGTGCATTTGCCCTCCACATGTCACACACTGGTT 920
Db      247  ---GlyProProGlyAlaProGlyProAlaGlyProProGlySerArgGlyAspProGly 265
OY      921  CCTGCTGATGTATCGACAGCGCTGCCCTTTCAGCTGTACATGCGCTTCAGAGTCAACGT 980
Db      266  ProProGlyAlaHis----- 270
OY      981  GTACTTGGGGGCGCATCTGCTGAAAGACGCTGCGCTGCGCTGCGCTGCTGCTGCTCC 1040
Db      271  -----GlyProAlaGlyProGlyAla---HisGlyProAlaGlyProGlySerGly 286
OY      1041  GCGGCTGAGCGGTACGACAGTACAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1100
Db      287  AlHisGlyProAla-----GlyProGlySerGlyAlaHisGlyProAla 300
OY      1101  CGCCCTGCTGCGGACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160
Db      301  GlyProGlySerGlyAlaProGly-----ProAlaGlyProPro 312
OY      1161  GACACAGCATTCGAGTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1214
Db      313  GlySerArgGlyAspProGlyProProGlyAlaProGlyProAlaGlyProProGlySer 332
OY      1215  ACTGGAGACTCCCTACTACCTGCTGCTGCGCGGAGCGACGCTGCA---GGAAACAGCTCGG 1271


Db      333  ArgGlyAspProGlyProProGlyAlaPro---GlyProAlaGlyProProGlySerArgGly 352
OY      1272  CAGAGTGAACAACAGACAGACAGACAGACAGCCAGCGGAGCGGCTGGAG---CTGCT 1328
Db      352  yAspProGlyProProGlyAlaProGlyProAlaGlyProProGlySerArgGlyAspPr 372
OY      1329  GGGGCGCGCTGCGTGGGACAGCGCTACATACCTCCCTGCTGCTGCTGCTGCTGCTGCT 1388
Db      372  oGlyProProGly---AlaProGlyProAlaGlyProProGlySerArgGlyAspProGly 392
OY      1389  CACACAGGTGGGCTGCGGCAACGTGTCCGCCAACACAGGACAGACAGAGAAATCTTCAT 1448
Db      392  roProGlyAlaProGlyProAlaGlyProProGlySerArgGlyAspProGlyProProG 412
OY      1449  CTCCACCACTGCTATCGCGCGCTGATGACAGCGGTGTGTGTTGGAACTGACAGCGCAT 1508
Db      412  IyAlaProGlyProAlaGlyPro-----ProG 421
OY      1509  CATCCAGCGATGTACGCGCGCGCTTCTGTTACACAGCGGACAGCGGAGCT---GCG 1565
Db      421  IySerArgGlyAspPro---GlyProProGlyAlaProGlyProAlaGlyProProGlySer 440
OY      1566  CGACTACATCCGCAATCCA-----CGTATCCCAAGCGCGCTTCAAGCGGATGCT 1616
Db      441  ArgGlyAspProGlyProProGlyAlaProGlyProAlaGlyProProGlySerArgGly 460
OY      1617  GGAGTACTTCCAGGCGCACCTGGCGGTGAAACATGTCATGCAACAGACAGAGTGTGCA 1676
Db      461  Asp-----ProGlyProProGlyAlaPro-----GlyProAla 471
OY      1677  GAGCTCCCTGACAGACTGCGCGGACAGATCCGATGACATGACACAGAGAGTCTGCA 1736
Db      472  GlyProPro-----GlySerArgGlyAspProGlyProProGlyAlaProAlaGlyPro 489
OY      1737  GGTGCCAGTGTGAGCGCGGACCGCGGCTGCTGCGGAGACTGTCTGTGCGCTGGCG 1796
Db      490  GlyProProGlySerArgGlyAspProGly---ProProGlyAlaProGly---ProAlaG 508
OY      1797  GCCGCGCTTGTGACGCGCGGAGATGCTATCCACCAAGCGGATGCTGACAGCGCT 1856
Db      508  IyProProGlySerArgGly---GlyAspProGlyProProGlyAlaHisGlyProAlaGlyPro 527
OY      1857  CTACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1910
Db      528  -----LysGlyAlaHisGlyProAlaGlyProLysGlyAlaHisGlyProAla 543
OY      1911  CATCTAGG-----GAAGGCGGACGTGATGCTGTGAGCT 1946
Db      544  GlyProLysGlyAlaHisGlyProAlaGlyProLysGlyAlaPro----- 558
OY      1947  GCCCGCGGGA---GAGTGTGTAAGCGCAATCCGACGTGAAAGGAGTGAACCTAGCTAG 2003
Db      559  GlyProAlaGlyProProGlySerArgGlyAspProGlyProProGlyAlaProGlyPro 578
OY      2004  CGTCTGAGTGTGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2063
Db      579  AlaGlyProProGlySerArgGlyAspProGlyProProGlyAlaProGlyProAlaGly 598
OY      2064  TGCCCGCGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2120
Db      599  ProProGlySerArgGlyAspProGlyProProGlyAla-----ProGlyProAla 615
OY      2121  GGAAGCTCTGACAGGTGACACAGCTCCCTGAGGCGGAGCAAAATCCATTATGTCCAC 2180
Db      616  GlyProProGlySerArgGlyAspProGlyProProGlyAlaProGlyPro----- 632
OY      2181  GCTGAGAGAGAGACAGATGGGAGACAGCGCGCGCTGCTCCAGCGCGAGCTGA 2240
Db      633  AlaGlyProProGlySerArgGlyAspProGlyProProGlyAlaProGlyProAlaGly 652
OY      2241  TGAGCTTCAGC-----CCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2267
Db      652  yProProGlySerArgGlyAspProGlyProProGlyAlaProGlyProAlaGlyProPr 672
```







```
QY 567 GTGCTTGCCCTTGCGCTCTCTGACAGTGCCGACAGTGAGACACGCG----- 514
Db 808 -----AlaProglyProAlaGlyProProglySerArg 818
QY 513 ---CGGCTCCGCGG-----CCGGTGGCATTTGAAGCCTTGATCGCGCG 469
Db 819 AspProglyProProglyAlaProglyProAlaGly-----Pro 831
QY 468 GCCATATCGGCGCGCGCA---CCACCTGTCTCTTCATCTGTGGGGGCCCCCTGCTT 412
Db 832 -ProglySerArgAspProglyProProglyAlaProglyProAlaGlyProPro-GlyS 851
QY 411 CTGGTTTCGTGATGTCTCTGTGAGAGACTGAGAGAGAGCA----- 368
Db 851 ex-----ArgAspProglyProProglyAlaP 860
QY 367 -----CCTCCCTTCTCATTTATGGGTATCATCCAGAGACACCA 322
Db 860 roglyProAlaGlyProProglySerArgAsp-----ProglyProProG 875
QY 321 GAGGAGAGCGCGCTCTCCGATACAGATCAGCTTGAACCTTGTGTCTGCTG 262
Db 875 lYAlaProglyProAlaGlyProProglySerArgAspProglyProProglyAla---P 894
QY 261 CAGGCGCTTCGCGATCTGTGGCGGACGACTCAGCTGTGTGGCCCATAAAGAGAGA 202
Db 894 roglyProAlaGlyProProglySerArg----- 903
QY 201 GCAGGACACGCCCGCTGCATGACCTCAGCCCGGAGAGCCGCTGAGGTCAAGAAACC 142
Db 904 --AspProglyProProglyAlaProglyProAlaGlyProPro--GlySerArgAspP 922
QY 141 ATCAGACAGTAGACACAGGAGAGAGCCCGCAGCTGGGCGTGGCCACAGCAAGTT 82
Db 922 roglyProProglyAlaProglyProAlaGlyProProgly----- 935
QY 81 ACTGTGCGTCCGTCGAGAGCGCGTAGCGATGTGTCCAGAAAGTGTCTGAGGCGCCAG 22
Db 936 -----SerArgAspProG 940
QY 21 GA-----GGCCCCGCGATGGCGG 5
Db 940 lYProProglyAlaAlaGlyProAlaGlyPro 950
```

Search completed: May 7, 2003, 15:27:03  
Job time : 122 secs